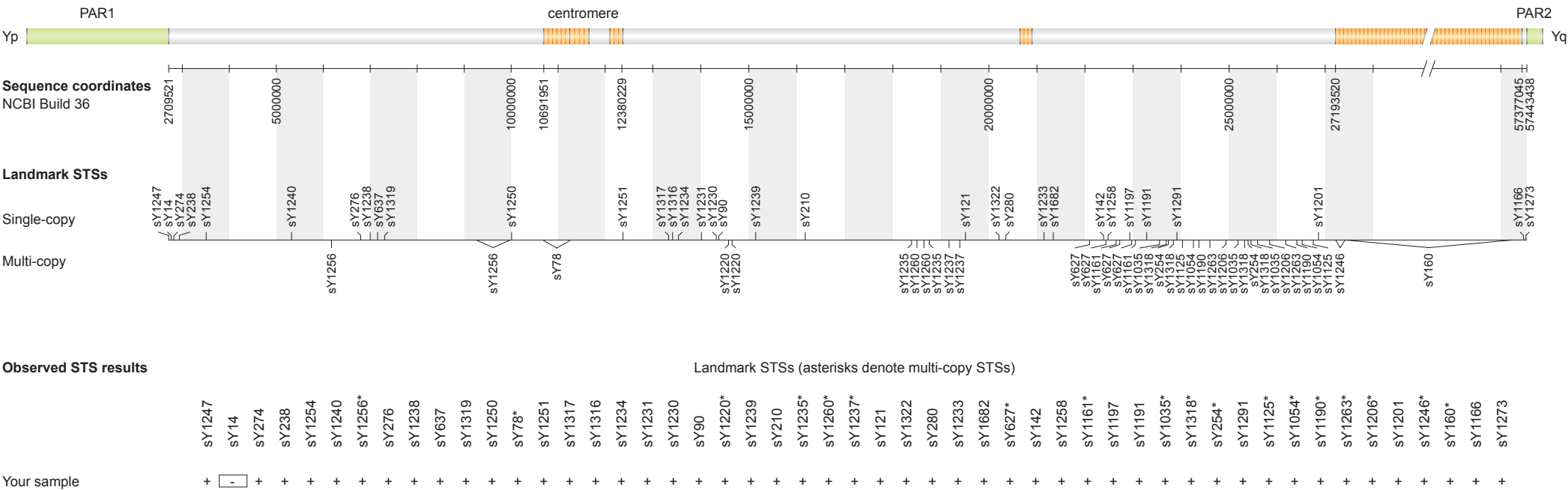


Example: Retrieve STSs Near One Locus

1. By testing your sample with 51 landmark STSs,¹ you have identified the following result: absence of a single STS, sY14.



2. To confirm the result for sY14 and to further delineate the deletion in your sample, you wish to assay additional STSs in the vicinity of sY14. To generate a catalog of STSs in a 50-kilobase interval surrounding sY14, select [sY14] and [50 kb] from pull-down menus, and click on the [Get STSs within interval] button.

Reference Tools

Table of landmark STSs

STS maps of common interstitial deletions

Retrieve STSs Between Two Loci

Landmark STSs Select to Select

Any two STSs Select to Select

chrY coordinates* to

Output format ☒ html ☐ text

*NCBI Build 36 Get intervening STSs Clear

Retrieve STSs Near One Locus

Landmark STS sY14 and 50 kb

Any one STS Select and Select interval

chrY coordinate* and Select interval

Output format ☒ html ☐ text

*NCBI Build 36 Get STSs within interval Clear

continued page 2

Notes

¹ See Table of landmark STSs under Reference Tools. Landmark STSs consist of sY1247 and sY1273, located at the boundaries between MSY and pseudoautosomal (PAR) sequences on Yp and Yq, respectively, and a previously published panel of 49 STS (see Supplementary Methods Table SM-2 in Repping et al., 2006).

3. STSs in the 50-kb interval surrounding sY14 are displayed as a table and in a custom Y chromosome browser. For each STS, the table indicates: multi-copy with an asterisk, start and end sequence coordinates, PCR product length, primer sequences, amplification conditions, GenBank accession number, and in the case of a multi-copy STS, sequence coordinates of co-amplified loci. The custom Y chromosome browser displays the 50-kb region encompassing the catalogued STSs. The position of each STS and of each protein-coding gene within the interval is indicated.

The following STSs are within chrY:2690575-2740574:

STS Identifier	Multi-copy	STS Start	STS End	STS Length	Primer 1	Primer 2	PCR Conditions	GenBank	Co-amplified Loci
sY1247		2709521	2709952	432	GAAGCTCTGCAAACTCCTGG	TTTGTAGGCGGAGTCTCG	Standard PCR	G75493	
SRY-1-5		2714797	2715594	798	CAGTCCAGCTGTGCAAGAGA	ATAGGCAGGCTCACTTCTGG	Touchdown PCR	BV679099	
SRY-1-6		2715010	2715695	686	TTTCGAAGCTCTGGCACCTT	GCCAATGTTACCCGATTGTC	Touchdown PCR	BV679100	
sY14		2715341	2715810	470	GAATATTCCTCGCTCTCCGGA	GCTGGTGCTCCATTCTTGAG	Standard PCR	G38356	
SRY-1-4		2715455	2716244	790	AGCCATCCTAGAAGTTGGGC	TGGGTCGCTTCACTCTATCC	Touchdown PCR	BV679098	
SRY-1-3		2715969	2716764	796	AGGAATTGTGGCATCATTAG	TCACAAAACGAGAGGACACAA	Touchdown PCR	BV679097	
SRY-1-2		2716624	2717313	690	TCCCCACAACCTCTTTCATC	AAATGGGAGGAAAGTCCCC	Touchdown PCR	BV679096	
SRY-1-1		2717134	2717907	774	CGCTGTACCTCTCCATAGCC	AAATGACACAAGGCACCACA	Touchdown PCR	BV679095	
SRY-flank-4		2719239	2720033	795	CCCAACATCTTGAAGGACA	GGGCTTAACCAACAGCAAAA	Touchdown PCR	BV679094	
SRY-flank-3		2719848	2720513	666	TGAAACCTTGTTTTACAGGCA	GCAGGTCACCAAGACACAA	Touchdown PCR	BV679093	
SRY-flank-2		2720286	2721050	765	GATTTGACCAAGCCTTTGGA	ATGAAGTAGGGTGCAAGTGGG	Touchdown PCR	BV679092	
SRY-flank-1		2720869	2721618	750	CCAAAGCTATGAGAGAGGCAG	CAGCAGCTGTTTGACCAAGA	Touchdown PCR	BV679091	
sY2045		2723295	2723399	105	AGCTTAACTGGTGTGCT	GAACCTAAAGTGACGAT	Standard PCR	G66044	
sY2901		2724300	2724522	223	GATTATGGGCCGAAATAGCA	GAATACAGCCCTTTGGTCA	Standard PCR	BV703768	

Showing 50 kb chrY:2690575-2740574

Instructions: Search using an STS identifier, sequence coordinates, or gene symbol. Gene symbols may require a final asterisk wildcard to indicate a gene copy. You can also specify a gene (Gene:BPY2*) or an STS (STS:BPY2*).
Examples: Y, Y:20000000..20100000, sY14, sY34, sY1229, AMELY, AMELY-4, DAZ*, sY*, Gene:BPY2*, STS:BPY2*, Gene:*

